

Supplemental Table 1. Identified proteins in 2D-DIGE of normal mouse liver lysate

Spot #	Protein ID	Comment
139	Pyruvate carboxylase, mitochondrial	Q05920; PI=6.10, MW=121.45 kDa
143	Pyruvate carboxylase, mitochondrial	Q05920; PI=6.12, MW=121.45 kDa
144	Pyruvate carboxylase, mitochondrial	Q05920; PI=6.16, MW=121.45 kDa
148	Pyruvate carboxylase, mitochondrial	Q05920; PI=6.16, MW=120.00 kDa
210	GRP94/ERP99	P08113; PI=4.88, MW=89.68 kDa
220	Tumor rejection antigen gp96	Q91V38; PI=4.7, MW=92.76
224	Alpha actinin 4; alpha actinin 2	0.042; Q8BP35; PI=5.2, MW=105.42 kDa; PI=5.3, MW=104.49
226	Alpha actinin 4; alpha actinin 2	0.042; Q8BP35; PI=5.2, MW=105.42 kDa; PI=5.3, MW=104.49
257	10-formyltetrahydrofolate dehydrogenase	Q8R0Y6; PI=5.42, MW=90.60 kDa
264	10-formyltetrahydrofolate dehydrogenase	Q8R0Y6; PI=5.52, MW=90 kDa
265	10-formyltetrahydrofolate dehydrogenase	Q8R0Y6; PI=5.77, MW=90 kDa
269	10-formyltetrahydrofolate dehydrogenase	Q8R0Y6; PI=5.61, MW=90 kDa
271	similar to KIAA1630 protein	0.005; Q9HCE2; PI=6.5, MW=96.95 kDa
273	similar to KIAA1630 protein	Q9HCE2; PI=6.5, MW=96.95 kDa
275	similar to KIAA1630 protein	Q9HCE2; PI=6.5, MW=96.95 kDa
282	Valosin-containing protein	0.014; Q9DBY8; PI=5.1, MW=89.97 kDa
291	Iron-responsive element binding protein 1 (IRE-BP 1) (Ferritin repressor protein)	P28271; PI=6.75, MW=99.50 kDa
309	SPTR	0.000; PI=5.5, MW=90.35 kDa
310	Sarcosine dehydrogenase	0.000; Q8BU72; PI=6.3, MW=102.69 kDa
312	SPTR	0.000; PI=5.5, MW=90.35 kDa
315	SPTR	0.000; PI=5.5, MW=90.35 kDa
319	Similar to Interferon-inducible protein 10 (IP10) receptor/Valosin containing protein	P17515; PI=5.1, MW=89.46 kDa
322	Sarcosine dehydrogenase	Q8BU72; PI=6.3, MW=102.69 kDa
353	Dimethylglycine dehydrogenase, mitochondrial	Q9UI17; PI=6.59, MW=82.90 kDa
354	Dimethylglycine dehydrogenase, mitochondrial	Q9UI17; PI=6.59, MW=82.90 kDa
355	Dimethylglycine dehydrogenase, mitochondrial	Q9UI17; PI=6.59, MW=82.90 kDa
371	Hsp 90-beta/Hsp 84	P11499; PI=5.02, MW=82.31 kDa
432	Iron-responsive element binding protein 1 (IRE-BP 1) (Ferritin repressor protein)	P28271; PI=6.84, Mw=89.04 kDa
473	Transferrin	PI=6.94, MW=76.67 kDa
475	Transferrin	PI=6.94, MW=76.67 kDa
485	similar to NADH-ubiquinone oxidoreductase 75 kDa subunit, mitoch	P28331; PI=5.5, MW=80.79
493	Transferrin	PI=6.94, MW=76.67 kDa
512	Transferrin	0.022; Q62375; PI=7.0, MW=78.83 kDa
537	Transferrin	0.022; Q62375; PI=7.0, MW= 78.83 kDa
540	GRP 78	0.010; P20029, PI=4.99, 5.01, 5.04,
557	GRP 75	0.007; P38647; PI=5.29, MW=69.43 kDa
562	GRP 75	0.007; P38647; PI=5.32, MW=69.06 kDa
567	GMP synthase	P49915; PI=6.3, MW=77.45
569	GRP 75	0.017; P38647; PI=5.34, MW=68.69 kDa
586	GRP 75	0.017; P38647
597	Hsc 71	0.004; P08109; PI=5.25, MW=67.78 kDa
599	Far upstream element (FUSE) binding protein 1	Q91WJ8; PI=7.8, MW=68.69 kDa
606	Hsc 71	0.004; P08109; PI=5.27, MW=67.42
618	Hsc 71	0.004; P08109; PI=5.30, MW=67.06 kD

629	Serum albumin	0.000; P07724; PI=5.68, MW=66.71 kDa
630	Serum albumin	0.000; P07724; PI=5.79, MW=66.53 kDa
637	Serum albumin	P07724; PI=5.37, MW=66.29 kDa
638	Serum albumin	P07724;
639	Serum albumin	P07724;
654	Transketolase	P40142; PI=6.5, MW=61.14
667	Lamin B1	P14733; PI=5.20, MW=65.51 kDa
671	Matrix metalloproteinase 14	Q8BTX2; PI=7.2, MW= 66.20 kDa
678	Serum albumin	P07724;
692	Dihydrolipoamide S-acetyltransferase	0.000; Q91ZB1; PI=5.7, MW=59.19 kDa
723	Stress induced phosphoprotein 1	P31948; PI=6.4, MW= 63.19 kDa
743	Ras -GTPase-activating protein SH3-domain binding protein	P97379; P97855; PI=5.4
752	similar to DKFZP586B 1621 protein	Q80VQ5; PI=6.4, MW=59.96 kDa
753	Heterogeneous nuclear ribonucleoprotein L	P14866;
766	Vimentin	P20152; PI=5.16, MW=59.61 kDa
767	2-hydroxyphytanoyl-CoA lyase (2-HPCL)	0.030; Q9QXE0; PI=5.9, MW=64.61 kDa
785	Calreticulin	P14211; PI=4.44, MW=59.61 kDa
792	Stress induced phosphoprotein 1, IEF SSP 3521	P31948; PI=6.4, MW=63.19 kDa
798	Heterogeneous nuclear ribonucleoprotein K isoform a	Q07244; PI=5.2
799	Phosphoglucomutase	Q9D0F9; PI=6.2, MW=60.05
809	T-complex protein 1, epsilon subunit (TCP-1-epsilon)	0.005; P11983; PI=5.74, MW=59.31
810	T complex polypeptide 1	0.005; P11983; PI=6.3, MW=57.97 kDa
813	Delta-1-Prroline-5-carboxylate-dehydrogenase; similar to aldehyde dehydrogenase 4 family, member A1	0.000; Q8BXM3; PI=8.8, MW=62.28 kDa; PI=8.6, MW=60.78 kDa
826	Delta-1-Prroline-5-carboxylate-dehydrogenase; similar to aldehyde dehydrogenase 4 family, ALDH4A1	0.000; Q8BXM3; PI=8.8, MW=62.28 kDa; PI=8.6, MW=60.78 kDa
837	Delta-1-Prroline-5-carboxylate-dehydrogenase; similar to aldehyde dehydrogenase 4 family, ALDH4A1	Q8BXM3; PI=8.8, MW=62.28 kDa; PI=8.6, MW=60.78 kDa
840	Hsp 60	0.000; P19226; PI=5.26, MW=58.29 kDa
841	Delta-1-Prroline-5-carboxylate-dehydrogenase; similar to aldehyde dehydrogenase 4 family, ALDH4A1	Q8BXM3; PI=8.8, MW=62.28 kDa; PI=8.6, MW=60.78 kDa
843	Chaperonin subunit 5 (epsilon)	Q8C5Q5; PI=5.7, MW=60.06 kDa
844	ALDH4A1	
848	Hsp 60	0.001; P19226; PI=5.29, MW=58.14
857	Alpha-1-antitrypsin	P07758; PI=4.92, Mw=56356
858	Hsp 60	0.000; P19226; PI=5.31, MW=58 kDa
864	Delta-1-Prroline-5-carboxylate-dehydrogenase; similar to aldehyde dehydrogenase 4 family, member A1	Q8BXM3; PI=8.8, MW=62.28 kDa; PI=8.6, MW=60.78 kDa
868	Alpha 1-antitrypsin	P07758;
872	Protein disulfide isomerase (PDI), ERP59	P09103; PI=4.82, MW=55.80 kDa
883	Protein disulfide isomerase (PDI), ERP59	P09103; PI=4.88, MW=55.50 kDa
885	Protein disulfide isomerase (PDI), ERP59	P09103; PI=4.86, MW=55.50 kDa
889	Protein disulfide isomerase A3 (ERp60), GRP58	P27773; PI=5.83, MW=56.42 kDa
891	Protein disulfide isomerase A3 (ERp60), GRP58	P27773; PI=5.70, MW=56.42
897	Protein disulfide isomerase A3 (ERp60), GRP58	P27773; PI=5.70, MW=56.42
925	Catalase	P24270; PI=8.3, MW=60.00 kDa
928	Catalase	P24270; PI=7.72, MW=59.727 kDa
929	Catalase	P24270; PI=8.3, MW=60.00 kDa

936	Cytoskeratin	PI=5.72, MW=54.59 kDa
937	Nuclear matrix protein SNEV	0.032; Q9UMS4; PI=6.1, MW=55.68 kDa
954	Tubulin alpha-1 chain	P02551; PI=5.11, MW=53.54 kDa
956	3-hydroxy-3-methylglutaryl-CoA synthase 1	0.004; P54869; PI=5.6, MW=58.16
958	Alpha-1-antitrypsin	P07758, PI=5.08, MW=54.18 kDa
970	Selenium-binding protein 1	P17563; PI=5.46, MW=53.25
973	Keratin 8	P11679; PI=5.54, MW=53.25
975	Glutamate dehydrogenase	P26443; PI=8.3, MW=61.66 kDa
978	Keratin 8	0.000; P11679;
984	Keratin 8	0.001; P11679; PI=5.69, MW=53.10 kDa
997	Methylmalonate-semialdehyde dehydrogenase	Q9EQ20; PI=8.7, MW=58.35 kDa
1008	Selenium binding protein 1	P17563; PI=5.62, MW=52.81
1009	Methylmalonate-semiacidhyde dehydrogenase	Q9EQ20;
1012	Selenium binding protein 1	P17563; PI=5.79, MW=52.67
1015	Glutamate dehydrogenase, mitochondrial	P26443; PI=6.56, MW=51.80 kDa
1018	Selenium binding protein 1	0.000; P17563; P17563; PI=5.92, MW=52.81
1020	Glutamate dehydrogenase	P26443; Q8C273; PI=6.47, MW=52.08
1030	ATP synthase, alpha subunit	0.058; Q03265; PI=9.3, MW=59.85 kDa
1036	ATP synthase beta chain	P56480; PI=5.10, MW=56.36 kDa
1046	Glutamate dehydrogenase	P26443; PI=6.69, MW=51.51 kDa
1052	ATP synthase beta chain	P56480; PI=5.1, MW=56.36
1063	Aldehyde dehydrogenase, mitochondrial	P47738; PI=6.15, Mw=50527
1070	Glutamate dehydrogenase	Q8C273; PI=6.77, MW=51.23 kDa
1075	K8 (without N-terminus)	0.008; P11679; PI=5.4, MW=53.33
1078	Aldehyde dehydrogenase, mitochondrial	P47738; PI=6.31, Mw=49972
1079	Aldehyde dehydrogenase, mitochondrial	P47738; PI=6.34, Mw=49972
1088	Septin 6	Q9R1T4; PI=5.9, MW=52.86
1089	ATP synthase beta chain	P56480
1102	Dihydrolipoamide branched chain transacylase	0.000; MW=53.48K
1105	Phenylalanine hydroxylase	0.000; P16331;
1119	Serine hydroxymethyltransferase	0.014; P50431; PI=6.5, MW=53.08
1123	Protein disulfide isomerase-related protein	Q922R8; PI=5.0, MW=49.07
1143	Ubiquinol-cytochrome C reductase core protein 1	P31930; PI=5.8, MW=53.44
1144	Proteasome 26S ATPase subunit 4	0.047; PI=5.1, MW=47.5 kDa
1147	Alpha enolase (Enolase 1)	P45376; PI=6.15, MW=47.16
1149	K18	P05784;
1152	Alpha enolase (Enolase 1)	P45376; PI=5.92, MW=47.16
1157	K18	P05784;
1160	K18	P05784;
1161	Alpha enolase (Enolase 1)	P45376; PI=6.34, Mw=46771
1163	HMG-CoA synthase	P54869, MW=53.7517 kD, PI=8.02
1165	Methionine adenosyltransferase I, alpha	PI=5.51, MW=43.51 kDa
1173	Hydroxymethylglutaryl-CoA synthase	P54869, MW=53.7517 kD, PI=8.02
1176	Elongation factor 1-alpha	P10126;
1181	Hydroxymethylglutaryl-CoA synthase	P54869; PI=7.7, MW=53.13 kDa
1189	Ornithine aminotransferase, mitochondria	0.000; P29758; PI=5.87, MW=47.55
1190	Ubiquinol-cytochrome-C reductase complex core protein I, mt	P31930, MW=52.5854 kD, PI=5.94
1201	2-oxoisovalerate dehydrogenase alpha subunit, mitochondrial	P50136; PI=5.94, MW=44.63

1211	Glutamine synthetase	P15105; PI=6.50, MW=44.63 kDa
1212	Argininosuccinate synthetase 1	P16460; PI=8.5, MW=46.85 kDa
1228	K8 fragment	
1237	Onithine aminotransferase	0.000; P29758; P29758; PI=6.2, MW=48.74 kDa
1256	Branched chain ketoacid dehydrogenase E1, alpha polypeptide	Q99L69; PI=8.4, MW=50.63 kDa
1257	Ornithine aminotransferase	0.01; P29758; PI=5.88, Mw=44.26 kDa
1263	Argininosuccinate synthetase (Citrulline-aspartate ligase)	P16460; PI=8.36, MW=46.55 kDa
1264	Endo A' Keratin	
1267	Keratin 18	P05784
1278	Keratin 18	P05784
1294	Adenosylhomocysteinase	P50247, MW=47.512 kDa, PI=5.97
1298	Beta-actin	P02570
1299	Adenosine kinase	MW= 37.29 kDa, PI=6.27
1301	Ornithine aminotransferase	P29758; PI=5.87, Mw=43.29 kDa
1302	Fumarylacetoacetate	P35505; PI=6.58, MW=43.65 kDa
1307	Fumarylacetoacetate	P35505
1309	Argininosuccinate synthetase 1	P16460; PI=8.5, MW=46.85 kDa
1322	Argininosuccinate synthetase 1	P16460
1323	Acetyl-CoA acetyltransferase 2	0.000; P24752, Q93YW6
1326	Succinyl-CoA ligase	Q9Z2I8
1328	Beta-actin	P02570; PI=5.14, MW=44.26 kDa
1335	Lamin receptor 1	P14206; Q8BNL2
1337	Lamin receptor 1	P14206; Q8BNL2
1340	Lamin receptor 1	P14206; Q8BNL2; PI=4.8, MW=32.93 kDa
1347	Succinyl-CoA ligase	Q9Z2I8
1354	Septin 2	P42208; PI=6.1, MW=41.74 kDa
1357	Isocitrate dehydrogenase	O88844; PI=6.50, MW=42.12 kDa
1361	Glycine C-acetyltransferase	Q9CZ08
1372	Aminoacylase 1	Q91XE4; PI=5.8
1382	Isovaleryl-CoA dehydrogenase, mitochondrial	P26440; PI=6.43, MW=41.17 kDa
1384	Haptoglobin	Q61646
1405	Fumarylacetoacetate	P35505; PI=6.71, Mw=40985
1407	Haptoglobin	Q61646
1412	Aspartate aminotransferase	P05201; PI=6.85, MW=40.44 kDa
1413	Proteasome 26S ATPase subunit 6	Q99JI4; PI=7.1, MW=44.44 kDa
1416	Fumarylacetoacetate	P35505; pi=6.77, Mw=40985
1418	Cytokeratin	
1421	Septin 2	P42208; PI=6.1, MW= 41.74 kDa
1422	HMG CoA synthase	P54869; PI=7.9, MW=48.4 kDa
1435	Haptoglobin	Q61646
1436	Poly(rC) binding protein 1	P60335; PI=6.7, MW=37.92 kDa
1467	Arginase 1	0.008; Q61176; PI=6.49, Mw=38425
1471	Haptoglobin	Q61646
1474	Keratin 8 fragment	
1478	Sorbitol dehydrogenase 1	Q64442; PI=6.6, MW=38.8 kDa
1507	Farnesyl pyrophosphate synthase	P49351
1518	Farnesyl pyrophosphate synthase	P49351
1529	Calponin 3, acidic isoform	0.000; Q15417

1531	Arginase 1	Q61176; PI=6.5, MW=34.96 kDa
1532	Eukaryotic translation initiation factor 3, subunit 2 (beta)	Q9QZD9; PI=5.4, MW=34.90 kDa
1554	Fructose bisphosphatase 1	P09200; PI=6.2, MW=37.29
1559	Fructose bisphosphatase 1	P09200; PI=6.2, MW=37.29 kDa
1561	Eukaryotic translation initiation factor 3, subunit 2 (beta)	Q9QZD9; PI=5.4, MW=34.90
1563	Alcohol dehydrogenase	Q9JII6; PI=6.85, MW=37.25 kDa
1578	F-actin capping protein alpha-1 subunit	P47753; PI=5.3, MW=32.90
1590	Ornithine carbamoyltransferase	P11725; PI=6.80, MW=36.51 kDa
1606	Aldose reductase	0.000; P45376; PI=6.7, MW=36.04 kDa
1616	Heterogeneous nuclear ribonucleoprotein A2	O88569; PI=8.7, MW=36.03
1642	Senescence marker protein-30	Q64374; PI=5.00, MW=34.23 kDa
1643	Senescence marker protein-30	Q64374; PI=4.96, MW=34.15 kDa
1659	RIKEN cDNA 2010317E03	PI=5.4, MW=33.11 kDa
1674	Glycerol phosphate dehydrogenase 1	0.000; P13707, Q8CBX6; PI=6.3, MW=35.57 kDa
1678	Albumin 1, alpha-fetoprotein, fragments	P02772, Q8C7H3; PI=5.5, MW=48.81
1699	Lactate dehydrogenase	P06151; PI=7.8, MW=36.82 kDa
1710	26S proteasome-associated pad1 homolog	Q9CZY6; PI=6.2, MW=34.72
1720	RIKEN cDNA 2010317E03	PI=5.4, MW=33.11 kDa
1724	Ketohexokinase	P97328; PI=5.68, MW=30.61 kDa
1729	Hydroxymethylglutaryl-CoA lyase	
1736	Glycine N-methyltransferase	Q8C4E3; PI=7.1, MW=32.65kDa
1775	Annexin V	P48036; MW=35.73kD, PI=4.83
1776	Annexin V	P48036; MW=35.73kD, PI=4.83
1791	Serine hydroxymethyltransferase	P50431; PI=6.78, MW=32.06 kDa
1803	3-hydroxyanthranilate 3,4-dioxygenase	P46952; PI=6.3, MW=25.61 kDa
1809	Keratin 1	Q61765
1817	Enoylcoenzyme A hydratase 1	Q8BH95
1823	Voltage-dependent anion-selective channel protein 1	Q60932; PI=8.7, MW=32.96 kDa
1825	Annexin VI, Annexin A4	0.001; P97429; PI=5.4, MW=36.26 kDa
1826	Apolipoprotein E	P08226)
1827	Voltage-dependent anion channel 2	Q60931; PI=7.7, MW=32.34
1834	RIKEN cDNA 3110049J23	PI=5.2, MW=32.19
1849	Glutathione S-transferase Yc	P30115; PI=6.59, MW=30.36
1866	3-hydroxyanthranilate 3,4-dioxygenase	P46952
1873	Tropomyosin 5	P21107
1904	Tropomyosin alpha 3 chain	P21107; PI=4.65, MW=28.07 kDa
1908	Prohibitin	P24142; PI=5.6, MW=29.53
2010	Phosphoglycerate mutase 1	Q9DBJ1; PI=6.2, MW=29.03 kDa
2034	Carbonic anhydrase III	P16015; PI=6.84, MW=27.86 kDa
2036	Carbonic anhydrase III	P16015; PI=6.98, MW=29.35
2039	Carbonic anhydrase III	P16015; PI=6.74, MW=27.91 kDa
2047	Electron-transfer-flavoprotein, beta polypeptide	PI=8.24, MW=27.83 kDa
2049	Cytochrome c oxidase polypeptide II	P00405; PI=4.72, MW=26.71 kDa
2057	Cathepsin D	P18242; PI=5.50, MW=27.85 kDa
2065	Enoyl Coenzyme A hydratase, short chain	Q8BH95; PI=9.2, MW=31.86
2086	Triosephosphate isomerase	Q64513; PI=6.94, MW=26.71 kDa
2092	Keratin 10 (or Endoplasmic reticulum protein ERp28), Peroxiredoxin 4	P02535; O08807; PI=5.66, MW=26.45 kDa; PI=6.7, MW=31.26 kDa

2095	Enoylcoenzyme A hydratase 1	Q8BH95; PI=5.92, MW=26.55 kDa
2096	Enoylcoenzyme A hydratase 1	Q8BH95; PI=5.57, MW=26.16 kDa
2103	GST mu type 3	PI=6.84, MW=25.66 kDa
2109	Glutathione S-transferase Mu 1	P10649; PI=7.25, Mw=26.32 kDa
2110	Glutathione S-transferase Mu 1	P10649; PI=7.35, Mw=26879
2115	Glutathione S-transferase Mu 1	P10649; PI=8.06, Mw=27106
2125	Glutathione S-transferase Mu 1	P10649; PI=7.25, Mw=26321
2127	Glyoxalase 1	PI=5.24, MW=20.8 kDa
2135	Translationally controlled tumor protein (TCTP)	P14701; PI=4.81, MW=24.05
2143	GST alpha 3	PI=8.76, MW=25.34 kDa
2144	GST alpha 3	
2156	Glutathione S-transferase theta 1	Q64471; PI=6.88, MW=25.72 kDa
2159	Glutathione peroxidase	P11352; PI=6.7, MW=22.28 kDa
2160	Apolipoprotein A-1	0.000; Q00623
2165	Cathepsin B	P10605; PI=5.29, MW=24.56 kDa
2168	Apolipoprotein A-1	0.001; Q00623; PI=5.27, MW=24.20 kDa
2177	Hypothetical protein MGC37914	Q8VC73; PI=7.8, MW=24.35 kDa
2181	Manganese superoxide dismutase, GST P2	P09671
2187	RIKEN cDNA 1110038105	PI=5.2, MW=20.81 kDa
2207	Apolipoprotein A-1	Q00623; PI=5.27, MW=24.20 kDa
2211	Glutathione S-transferase P 2	PI=7.08, MW=24.87kDa
2217	ATP synthase D chain, mt	P31399, MW=18.62 kDa, PI=6.21
2220	GST P, GST pi2	PI=8.10, MW=23.47
2223	Glutathione S-transferase P 2	PI=7.39, MW=24.92 kDa
2235	Ferritin L chain	0.000; P29391
2247	Thioredoxin peroxidase 2	P35700, MW=22.162 kD, PI=8.26
2261	Superoxide dismutase	P09671; PI=7.21, Mw=24101
2281	Sodium channel mNa 2,3 voltage-gate	
2294	Major urinary protein 2, alpha-2u-globulin I	0.000; P11589; PI=4.88, Mw=19046
2298	Major urinary protein 2, alpha-2u-globulin I	0.008; P11589; PI=4.80, Mw=19046
2303	Major urinary protein 6, alpha-2u-globulin I	0.001; P02762
2304	Ferritin heavy chain	0.005; P09528